



OICE

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/843,676

TIME: 15:48:38

Input Set : N:\Crif3\RULE60\09843676.raw

Output Set: N:\CRF3\02062002\I843676.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Cech, Thomas R.
 6 Lingner, Joachim
 7 Nakamura, Toru
 8 Chapman, Karen B.
 9 Morin, Gregg B.
 10 Harley, Calvin
 11 Andrews, William H.

13 (ii) TITLE OF INVENTION: Novel Telomerase

15 (iii) NUMBER OF SEQUENCES: 225

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 19 (B) STREET: Two Embarcadero Center, 8th Floor
 20 (C) CITY: San Francisco
 21 (D) STATE: California
 22 (E) COUNTRY: United States of America
 23 (F) ZIP: 94111

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk
 27 (B) COMPUTER: IBM PC compatible
 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/843,676
 C--> 33 (B) FILING DATE: 26-Apr-2001
 54 (C) CLASSIFICATION: 536

51 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/854,050
 38 (B) FILING DATE: 09-MAY-1997
 42 (A) APPLICATION NUMBER: US 08/846,017
 43 (B) FILING DATE: 25-APR-1997
 47 (A) APPLICATION NUMBER: US 08/844,419
 48 (B) FILING DATE: 18-APR-1997
 52 (A) APPLICATION NUMBER: US 08/724,643
 53 (B) FILING DATE: 01-OCT-1996

56 (viii) ATTORNEY/AGENT INFORMATION:

57 (A) NAME: Apple, Randolph T.
 58 (B) REGISTRATION NUMBER: 36,429
 59 (C) REFERENCE/DOCKET NUMBER: 015389-002930US

61 (ix) TELECOMMUNICATION INFORMATION:

62 (A) TELEPHONE: (415) 576-0200
 63 (B) TELEFAX: (415) 576-0300

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65 (2) INFORMATION FOR SEQ ID NO: 1:

67 (i) SEQUENCE CHARACTERISTICS:

68 (A) LENGTH: 3279 base pairs

69 (B) TYPE: nucleic acid

70 (C) STRANDEDNESS: single

71 (D) TOPOLOGY: linear

73 (ii) MOLECULE TYPE: other nucleic acid

74 (A) DESCRIPTION: /desc = "DNA"

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

78	AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
80	TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120
82	TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180
84	TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240
86	TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG	300
88	AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360
90	AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA	420
92	TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA	480
94	TTTATTAACA GCTCTTTCAA CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT	540
96	TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600
98	GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA	660
100	AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720
102	ATGTTGATCA ACCTGCAAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT	780
104	CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT	840
106	TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT	900
108	AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960
110	GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT	1020
112	TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGAACGGAA	1080
114	ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA	1140
116	GCTGTTTAGC TACACAACCTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA	1200
118	CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT	1260
120	TAAGAAATAT GTGGAATAA ACAAGCATGA ACTCATTAC AAAAATTAT TGCTTGAGAA	1320
122	GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA	1380
124	TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT	1440
126	CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA	1500
128	AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT	1560
130	AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT	1620
132	TGGATTGCA CCTGGAAGAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT	1680
134	GACTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC	1740
136	GAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC	1800
138	TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTTG	1860
140	CAAAATGGAAG CAAGTTGGAC AACCAAAACCT CTTCTTTGCA ACTATGGATA TCGAAAAGTG	1920
142	ATATGATAGT GTAAACAGAG AAAAATATC AACATTCTTA AAACTACTA AATTACTTTC	1980
144	TTGAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA	2040
146	TTGAGAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT	2100
148	TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA	2160
150	CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA	2220
152	TAACTTACTT CAACCAAGTCA TTAATATTTG CCAATATAAT TACATTAAC TTAATGGGAA	2280
154	GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTGATC	2340
156	ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA	2400

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158 CCCTGAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC 2460
160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA 2520
162 TGGATTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT 2580
164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
166 GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
170 CAAGAAGAAA CTAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT 2820
172 TACAACCGAA GACTTTGCGA ATAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG 2940
176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT 3060
180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT 3120
182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT 3180
184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTGT 3240
186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG 3279

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188 (2) INFORMATION FOR SEQ ID NO: 2:

190 (i) SEQUENCE CHARACTERISTICS:

191 (A) LENGTH: 1031 amino acids

192 (B) TYPE: amino acid

193 (C) STRANDEDNESS: Not Relevant

W--> 194 (D) TOPOLOGY: Not Relevant

196 (ii) MOLECULE TYPE: protein

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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200 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
201 1 5 10 15
203 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
204 20 25 30
206 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
207 35 40 45
209 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
210 50 55 60
212 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
213 65 70 75 80
215 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
216 85 90 95
218 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
219 100 105 110
221 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
222 115 120 125
224 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
225 130 135 140
227 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
228 145 150 155 160
230 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
231 165 170 175
233 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
234 180 185 190
236 Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
237 195 200 205

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239   Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
240       210                215                220
242   Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
243   225                230                235                240
245   Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
246       245                250                255
248   His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
249       260                265                270
251   Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
252       275                280                285
254   Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
255       290                295                300
257   Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
258   305                310                315                320
260   Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
261       325                330                335
263   Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
264       340                345                350
266   Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
267       355                360                365
269   Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
270       370                375                380
272   Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
273   385                390                395                400
275   Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
276       405                410                415
278   Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
279       420                425                430
281   Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
282       435                440                445
284   Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
285       450                455                460
287   Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
288   465                470                475                480
290   Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
291       485                490                495
293   Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
294       500                505                510
296   Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
297       515                520                525
299   Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
300       530                535                540
302   Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
303   545                550                555                560
305   Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
306       565                570                575
308   Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
309       580                585                590
311   Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr

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312																
314	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys
315		610					615					620				
317	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg
318		625				630					635					640
320	Lys	Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met
321					645					650					655	
323	Lys	Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly
324				660					665					670		
326	Gln	Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu
327			675					680					685			
329	Asn	Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe
330		690					695					700				
332	Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn
333		705				710					715					720
335	Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro
336					725					730					735	
338	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr
339				740					745					750		
341	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro
342			755					760					765			
344	Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu
345		770					775					780				
347	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu
348		785				790					795					800
350	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
351					805					810					815	
353	Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met
354				820					825					830		
356	Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
357			835					840					845			
359	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
360		850					855					860				
362	Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr
363		865				870					875					880
365	Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
366					885					890					895	
368	Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
369				900					905					910		
371	Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
372			915	</												

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09843676.raw

Output Set: N:\CRF3\02062002\I843676.raw

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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L:7318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217